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REMARKS

Claims 1-4, 8, 9, and 14-16 are under consideration in this application Claims 1-4 8, 9 and 14-16 are rejected under 35 USC § 112 No new matter has been added.

Claim Rejections – 35 USC § 112, first Paragraph

Claims 10, 11, 15 and 16 are rejected under 35 USC § 112, 1st paragraph for failing to comply with the written description requirement.

Claims 10 and 11 have been canceled previously and therefore this rejection is moot with respect to those claims.

The examiner argues the claims lack a description of the yvaW promoter region in the specification and thus the chimeric gene recited in the claims fails the written description requirement. Applicants respectfully traverse.

By way of clarification, claims 15 and 16 are dependent upon claims 1 and 2, but do not independently recite a chimeric gene. Claims 1 and 2 are not a subject of the stated rejection. Applicants respond here on the assumption that the rejection is applicable to claims 1, 2 and those dependent thereon.

It is axiomatic that which is well known to the skilled person need not be disclosed in detail in order to meet the written description requirement. See for example MPEP 2163 IIA3(a) which states:

"What is conventional or well known to one of ordinary skill in the art need not be disclosed in detail. See Hybritech Inc. v. Monoclonal Antibodies, Inc., 802 F.2d at 1384, 231 USPQ at 94. If a skilled artisan would have understood the inventor to be in possession of the claimed invention at the time of filing, even if every nuance of the claims is not explicitly described in the specification, then the adequate description requirement is met. See, e.g., Vas-Cath, 935 F.2d at 1563, 19 USPQ2d at 1116; Martin v. Johnson, 454 F.2d 746, 751, 172 USPQ 391, 395 (CCPA 1972) (stating "the description need not be in ipsis verbis [i.e., "in the same words"] to be sufficient")." MPEP 2163 IIA3(a)

The examiner states that neither the prior art nor the specification teach the structural requirements of the promoter region of yvaWXY (page 3 of the present action). In fact, the genome of Bacillus subtilis was made available in 1997 in Nature 390 (6657), 249-256 (1997) and as Genbank accession number Z99121 AL009126 (partially reproduced below)

LOCUS BSUB0018 194692 bp DNA linear BCT 18-APR-2005 DEFINITION Bacillus subtilis complete genome (section 18 of 21): from 3414339 to 3609030. ACCESSION Z99121 AL009126 VERSION Z99121.2 GI:32468825 Application No.: 10/602747 Docket No.: CL1686USDIV

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KEYWORDS .
            Bacillus subtilis subsp. subtilis str. 168
SOURCE
 ORGANISM Bacillus subtilis subsp. subtilis str. 168
       Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE 1 (bases 1 to 194692)
 AUTHORS Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G.,
       Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S.,
       Borriss, R., Boursier, L., Brans, A., Bram, M., Brignell, S.C.,
       Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V.,
        Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J.,
       Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D.,
        Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E.,
        Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A.,
        Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightty, E.J.,
        Grandi, G., Gulseppi, G., Guy, B.J., Haga, K., Haiech, J., Harwood, C.R.,
        Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hullo, M.F.,
        Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y.,
        Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P.,
        Koningstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A.,
        Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, H.,
        Masuda,S., Mauel,C., Medigue,C., Medina,N., Mellado,R.P.,
        Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M.,
        Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M.,
        Portetelle, D., Porwollik, S., Prescott, A.M., Presecan, E., Pujic, P.,
        Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M.,
        Rivolta, C., Rocha, B., Roche, B., Rose, M., Sadaie, Y., Sato, T.
        Scanlan, E., Schleich, S., Schroeter, R., Scoffone, F., Sekiguchi, J.,
         Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B.,
         Sorokin, A., Tacconi, E., Takagi, T., Takahashi, H., Takemaru, K.,
         Takeuchi, M., Tamakoshi, A., Tanaka, T., Terpatra, P., Tognoni, A.,
         Tosato, V., Uchiyama, S., Vandenbol, M., Varmier, F., Vassarotti, A.,
         Viari, A., Wambutt, R., Wedler, E., Wedler, H., Weitzenegger, T.,
         Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K.,
         Yoshida,K., Yoshikawa,H.F., Zumstein,E., Yoshikawa,H. and
         Danchin, A.
   TITLE The complete genome sequence of the gram-positive bacterium
         Bacillus subtilis
   JOURNAL Nature 390 (6657), 249-256 (1997)
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48218..48760

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<u>CDS</u>

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NLEKQIKPIKVIKNEDYIHLSKGEYLIYRQKPLSWYWIDFKQTTSFERKVLKIKIV"

The above excerpt from the Genbank record of the full genome of Bacillus subtilis indicates that the coding region of yvaV ends at base 48760 and the coding region of yvaW begins at base 48982. The skilled person will recognize that the promoter region will lie upstream of the yvaW coding region prior to the start of the yvaV coding region and would easily be able to discern the portion of the genome containing the promoter region in question.

Applicants submit that the discovery of the invention was the finding that the yvaWXY promoter was activated in the absence of oxygen, and the person of skill in the art, looking to the teaching of the prior art in view of the specification would reasonably conclude that the applicant was in possession of the invention at the time the application was filed.

In view of the foreign Applicants respectfully request reconsideration of the claims as amended and removal of all rejections.

Respectfully submitted,

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Dated: January 9, 2006